



#8

SEQUENCE LISTING

<110> Scandinavian Biotechnology Research (ScanBi AB) AB, ORG. NO. 556577-8445

<120> USE OF A CLASS OF ENZYMES AND THEIR ENCODING GENES TO INCREASE THE OIL CONTENT IN TRANSGENIC ORGANISMS

<160> 2

<210> 1

<211> 1833

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 1

```
atgacggaga ctaaggattt gttgcaagac gaagagtttc ttaagatccg cagactcaat 60
tccgcagaag ccaacaaacg gcattcggtc acgtacgata acgtgacccg gccacaggag 120
tccatggagg ttctgccacg gtcgtctacc acgtcgtctg tggagccagt ggagtcgact 180
gaaggagtgg agtcgactga ggcggaacgt gtggcaggga agcaggagca ggaggaggag 240
taccctgtgg acgcccacat gcaaaagtac ctttcacacc tgaagagcaa gtctcggctc 300
aggttccacc gaaaggatgc tagcaagtat gtgtcgtttt ttggggacgt gagttttcat 360
cctcgcacca cgctcctgga cagcgccatc aacgtgccct tccagacgac tttcaaaggc 420
ccggtgctgg agaaacagct caaaaattta cagttgacaa agaccaagac caaggccacg 480
gtgaagacta cgggtgaagac tacggagaaa acggacaagg cagatgcccc cccaggagaa 540
aaactggagt cgaacttttc agggatctac gtgttcgcat ggatgttctt gggctggata 600
gccatcaggt gctgcacaga ttactatgct tcgtacggca gtgcatggaa taagctggaa 660
atcgtgcagt acatgacaac ggacttgctt acgatcgcaa tgttggaact ggcaatgttc 720
ctgtgcactt tcttcgtggt ttctgtgcac tggctggtga aaaagcggat catcaactgg 780
aagtggactg ggttcgttgc agtgagcatc ttccagttgg ctttcacccc cgtgacgttc 840
ccattttacg tctactactt tgatttcaac tgggtcacga gaatcttctt gttcctgcac 900
tccgtggtgt ttgttatgaa gagccactcg tttgcctttt acaacgggta tctttgggac 960
ataaagcagg aactcgagta ctcttccaaa cagttgcaaa aatacaagga atctttgtcc 1020
ccagagaccc gcgagattct gcaaaaaagt tgcgactttt gccttttcga attgaactac 1080
cagaccaagg ataacgactt ccccaacaac atcagttgca gcaatttctt catgttctgt 1140
ttgttccccg tctcgtgta ccagatcaac taccacaaga cgtcgcgcac cagatggagg 1200
tatgtgttgg agaaggtgtg cgccatcatt ggccaccatc tcctcatgat ggtcacggca 1260
cagttcttca tgcacccggt ggccatgctc tgtatccagt tccacaacac gccacacctc 1320
ggcggctgga tccccgccac gcaagagtgg ttccacctgc tcttcgacat gattccgggc 1380
ttcactgttc tgtacatgct cacgttttac atgatatggg acgctttatt gaattgcgtg 1440
gcggagttag ccagggtttg ggacagatat ttctacggcg actggtggaa ttgcgtttcg 1500
tttgaagagt ttagcagaat ctggaacgct cccgttcaca aatttttact aagacacgtg 1560
taccacagct ccattgggagc attgcatttg agcaagagcc aagctacatt atttactttt 1620
ttcttgagtg ccgtgttcca cgaaatggcc atgttcgcca ttttcagaag ggttagagga 1680
tatctgttca tgttccaact gtcgcagttt gtgtggactg ctttgagcaa caccaagttt 1740
ctacgggcaa gaccgcagtt gtccaacggt gtcttttctg ttggtgtctg ttcagggccc 1800
agtatcatta tgacgttgta cctgacctta tga 1833
```

<210> 2
<211> 610
<212> PRT
<213> *Saccharomyces cerevisiae*

·<400> 2

Met	Thr	Glu	Thr	Lys	Asp	Leu	Leu	Gln	Asp	Glu	Glu	Phe	Leu	Lys	Ile	1	5	10	15
Arg	Arg	Leu	Asn	Ser	Ala	Glu	Ala	Asn	Lys	Arg	His	Ser	Val	Thr	Tyr	20	25	30	
Asp	Asn	Val	Ile	Leu	Pro	Gln	Glu	Ser	Met	Glu	Val	Ser	Pro	Arg	Ser	35	40	45	
Ser	Thr	Thr	Ser	Leu	Val	Glu	Pro	Val	Glu	Ser	Thr	Glu	Gly	Val	Glu	50	55	60	
Ser	Thr	Glu	Ala	Glu	Arg	Val	Ala	Gly	Lys	Gln	Glu	Gln	Glu	Glu	Glu	65	70	75	80
Tyr	Pro	Val	Asp	Ala	His	Met	Gln	Lys	Tyr	Leu	Ser	His	Leu	Lys	Ser	85	90	95	
Lys	Ser	Arg	Ser	Arg	Phe	His	Arg	Lys	Asp	Ala	Ser	Lys	Tyr	Val	Ser	100	105	110	
Phe	Phe	Gly	Asp	Val	Ser	Phe	Asp	Pro	Arg	Pro	Thr	Leu	Leu	Asp	Ser	115	120	125	
Ala	Ile	Asn	Val	Pro	Phe	Gln	Thr	Thr	Phe	Lys	Gly	Pro	Val	Leu	Glu	130	135	140	
Lys	Gln	Leu	Lys	Asn	Leu	Gln	Leu	Thr	Lys	Thr	Lys	Thr	Lys	Ala	Thr	145	150	155	160
Val	Lys	Thr	Thr	Val	Lys	Thr	Thr	Glu	Lys	Thr	Asp	Lys	Ala	Asp	Ala	165	170	175	
Pro	Pro	Gly	Glu	Lys	Leu	Glu	Ser	Asn	Phe	Ser	Gly	Ile	Tyr	Val	Phe	180	185	190	
Ala	Trp	Met	Phe	Leu	Gly	Trp	Ile	Ala	Ile	Arg	Cys	Cys	Thr	Asp	Tyr	195	200	205	
Tyr	Ala	Ser	Tyr	Gly	Ser	Ala	Trp	Asn	Lys	Leu	Glu	Ile	Val	Gln	Tyr	210	215	220	
Met	Thr	Thr	Asp	Leu	Phe	Thr	Ile	Ala	Met	Leu	Asp	Leu	Ala	Met	Phe	225	230	235	240
Leu	Cys	Thr	Phe	Phe	Val	Val	Phe	Val	His	Trp	Leu	Val	Lys	Lys	Arg	245	250	255	
Ile	Ile	Asn	Trp	Lys	Trp	Thr	Gly	Phe	Val	Ala	Val	Ser	Ile	Phe	Glu	260	265	270	
Leu	Ala	Phe	Ile	Pro	Val	Thr	Phe	Pro	Ile	Tyr	Val	Tyr	Tyr	Phe	Asp	275	280	285	
Phe	Asn	Trp	Val	Thr	Arg	Ile	Phe	Leu	Phe	Leu	His	Ser	Val	Val	Phe	290	295	300	
Val	Met	Lys	Ser	His	Ser	Phe	Ala	Phe	Tyr	Asn	Gly	Tyr	Leu	Trp	Asp	305	310	315	320
Ile	Lys	Gln	Glu	Leu	Glu	Tyr	Ser	Ser	Lys	Gln	Leu	Gln	Lys	Tyr	Lys				

[illegible]